



SEQUENCE LISTING

RECEIVED
JAN 15 2002
TECH CENTER 160012900

<110> Croce, Carlo
<120> Nitrilase Homologs

<130> CRO01.NP001

<140> 09/357,675
<141> 1999-07-20

<150> 60/093,350
<151> 1998-07-20

<160> 25

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1416
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (19)...(19)
<223> n=a

<400> 1
gccactcgc tgcggcctnt ctggctccag accgcectcc ggatcggacc ctgcgaatgg 60
ttttggctat atcttcatgt aggacctact ccctatcccg tcggccgcgg ctgggcttca 120
tcaccaggcc tcctcacaga ttctgtccc ttctgtgtcc tggactccgg atacctcaac 180
tctcagtact ttgtgctcag ccaggccca gagccatggc tatctcctct tcctcctgcg 240
aactgcccc tgggtgctgtg tgccaggtaa catcgacgcc agacaagcaa cagaacttta 300
aaacatgtgc tgagctgggt cgagaggctg ccagactggg tgcttgctg gctttcctgc 360
ctgaggcatt tgacttcatt gcacgggacc ctgcagagac gctacacctg tctgaaccac 420
tggtgtgggaa acttttggaa gaatacacc agcttgccag ggaatgtgga ctctgggtgt 480
ccttgggtgg tttccatgag cgtggccaag actgggagca gactcagaaa atctacaatt 540
gtcacgtgct gctgaacagc aaaggggcag tagtggccac ttacaggaag acacatctgt 600
gtgacgtaga gattccaggg caggggccta tgtgtgaaag caactctacc atgcctgggc 660
ccagtcttga gtcacctgtc agcacaccag caggcaagat tgggtctagct gtctgctatg 720
acatgcggtt ccctgaactc tctctggcat tggctcaagc tggagcagag atacttacct 780
atccttcagc ttttggatcc attacaggcc cagccactg ggaggtgttg ctgcggggccc 840
gtgctatcga aaccacgtgc tatgtagtgg cagcagcaca gtgtggacgc caccatgaga 900
agagagcaag ttatggccac agcatgggtg tagaccctg gggaaacagt gtggcccgtc 960
gctctgaggg gccaggcctc tgccctgccc gaatagacct caactatctg cgacagttgc 1020
gccgacacct gcctgtgttc cagcaccgca ggccctgacct ctatggcaat ctgggtcacc 1080
cactgtctta agacttgact tctgtgagtt tagacctgcc cctcccacc ccacctgcc 1140
actatgagct agtgctcatg tgacttggag gcaggatcca ggcacagctc ccctcacttg 1200
gagaaccttg actctcttga tggaaacacag atgggctgct tgggaaagaa actttcacct 1260
gagcttcacc tgaggtcaga ctgcagtttc agaaagggtg aattttatat agtcattggt 1320
tatttcattg aaactgaagt tctgctgagg gctgagcagc actggcattg aaaaatataa 1380
taatcataaa gtcaaaaaaa aaaaaaaaaa aaaaaa 1416

<210> 2
 <211> 23
 <212> DNA
 <213> Homo sapiens

 <400> 2
 tctgaaactg cagtctgacc tca 23

 <210> 3
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 3
 caggcacagc tccccctcact t 21

 <210> 4
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (0)...(0)
 <223> n=a, g, c or t

 <400> 4
 gtngtncng gncaygtngt 20

 <210> 5
 <211> 26
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (0)...(0)
 <223> n=a,c,g, or t and y=c or t

 <400> 5
 acrtgnacrt gyttnacngt ytgngc 26

 <210> 6
 <211> 21
 <212> DNA
 <213> Drosophila melanogaster

 <400> 6
 gcgcctttgt ggcctcgact g 21

 <210> 7
 <211> 21
 <212> DNA
 <213> Drosophila melanogaster

<400> 7
 cggtggcgga agttgtctgg t 21
 <210> 8
 <211> 20
 <212> DNA
 <213> Caenorhabditis elegans
 <400> 8
 gtggcggtg ctcaaactgg 20
 <210> 9
 <211> 21
 <212> DNA
 <213> Caenorhabditis elegans
 <400> 9
 tcgcgacgat gaacaagtcg g 21
 <210> 10
 <211> 19
 <212> DNA
 <213> Homo sapiens
 <400> 10
 gccctccgga tcggaccct 19
 <210> 11
 <211> 20
 <212> DNA
 <213> Homo sapiens
 <400> 11
 gacctactcc ctatcccgtc 20
 <210> 12
 <211> 21
 <212> DNA
 <213> Homo sapiens
 <400> 12
 gctgcgaagt gcacagctaa g 21
 <210> 13
 <211> 24
 <212> DNA
 <213> Homo sapiens
 <400> 13
 aaactgaagc ctctttcctc tgac 24
 <210> 14
 <211> 20
 <212> DNA

<213> Homo sapiens
 <400> 14
 tgggcttcat caccaggcct 20
 <210> 15
 <211> 22
 <212> DNA
 <213> Homo sapiens
 <400> 15
 ctgggctgag cacaaagtac tg 22
 <210> 16
 <211> 21
 <212> DNA
 <213> Homo sapiens
 <400> 16
 gcttgtctgg cgtcgatgtt a 21
 <210> 17
 <211> 36
 <212> DNA
 <213> Homo sapiens
 <400> 17
 tgacgtcgac atatgtcaac tctagttaat accacg 36
 <210> 18
 <211> 25
 <212> DNA
 <213> Homo sapiens
 <400> 18
 tgggtacctc gactagctta tgtcc 25
 <210> 19
 <211> 147
 <212> PRT
 <213> Homo sapien
 <220>
 <223> Xaa is an unknown amino acid
 <400> 19
 Met Ser Phe Arg Phe Gly Gln His Leu Ile Lys Pro Ser Val Val Phe
 1 5 10 15
 Leu Lys Thr Glu Leu Ser Phe Ala Leu Val Asn Arg Lys Pro Val Val
 20 25 30
 Pro Gly His Val Leu Val Cys Pro Leu Arg Pro Val Glu Arg Phe His
 35 40 45
 Asp Leu Arg Pro Asp Glu Val Ala Asp Leu Phe Gln Thr Thr Gln Arg
 50 55 60
 Val Gly Thr Val Val Glu Lys His Phe His Gly Thr Ser Leu Thr Phe

65					70					75				80
Ser	Xaa	Gln	Asp	Gly	Pro	Glu	Ala	Gly	Gln	Thr	Val	Lys	His	Val
				85					90					95
Val	His	Val	Leu	Pro	Arg	Lys	Ala	Gly	Asp	Phe	His	Arg	Asn	Asp
			100					105					110	
Ile	Tyr	Glu	Glu	Leu	Gln	Lys	His	Asp	Lys	Glu	Asp	Phe	Pro	Ala
		115					120					125		
Trp	Arg	Ser	Glu	Glu	Glu	Glu	Ala	Ala	Glu	Ala	Ala	Ala	Leu	Arg
	130					135					140			
Tyr	Phe	Gln												
145														

<210> 20
 <211> 150
 <212> PRT
 <213> murine

<400> 20														
Met	Ser	Phe	Arg	Phe	Gly	Gln	His	Leu	Ile	Lys	Pro	Ser	Val	Val
1				5					10					15
Leu	Lys	Thr	Glu	Leu	Ser	Phe	Ala	Leu	Val	Asn	Arg	Lys	Pro	Val
			20					25					30	
Pro	Gly	His	Val	Leu	Val	Cys	Pro	Leu	Arg	Pro	Val	Glu	Arg	Phe
		35					40					45		
Asp	Leu	His	Pro	Asp	Glu	Val	Ala	Asp	Leu	Phe	Gln	Val	Thr	Gln
	50					55					60			
Val	Gly	Thr	Val	Val	Glu	Lys	His	Phe	Gln	Gly	Thr	Ser	Ile	Thr
65					70				75					80
Ser	Met	Gln	Asp	Gly	Pro	Glu	Ala	Gly	Gln	Thr	Val	Lys	His	Val
				85				90						95
Val	His	Val	Leu	Pro	Arg	Lys	Ala	Gly	Asp	Phe	Pro	Arg	Asn	Asp
			100					105					110	
Ile	Tyr	Asp	Glu	Leu	Gln	Lys	His	Asp	Arg	Glu	Glu	Glu	Asp	Ser
		115					120					125		
Ala	Phe	Trp	Arg	Ser	Glu	Lys	Glu	Met	Ala	Ala	Glu	Ala	Glu	Ala
	130					135					140			
Arg	Val	Tyr	Phe	Gln	Ala									
145					150									

<210> 21
 <211> 327
 <212> PRT
 <213> Homo sapien

<400> 21														
Met	Leu	Gly	Phe	Ile	Thr	Arg	Pro	Pro	His	Arg	Phe	Leu	Ser	Leu
1				5					10					15
Cys	Pro	Gly	Leu	Arg	Ile	Pro	Gln	Leu	Ser	Val	Leu	Cys	Ala	Gln
			20					25					30	
Arg	Pro	Arg	Ala	Met	Ala	Ile	Ser	Ser	Ser	Ser	Cys	Glu	Leu	Pro
		35					40				45			
Val	Ala	Val	Cys	Gln	Val	Thr	Ser	Thr	Pro	Asp	Lys	Gln	Gln	Asn
	50					55					60			

Lys	Thr	Cys	Ala	Glu	Leu	Val	Arg	Glu	Ala	Ala	Arg	Leu	Gly	Ala	Cys
65					70					75					80
Leu	Ala	Phe	Leu	Pro	Glu	Ala	Phe	Asp	Phe	Ile	Ala	Arg	Asp	Pro	Ala
				85					90					95	
Glu	Thr	Leu	His	Leu	Ser	Glu	Pro	Leu	Gly	Gly	Lys	Leu	Leu	Glu	Glu
			100					105					110		
Tyr	Thr	Gln	Leu	Ala	Arg	Glu	Cys	Gly	Leu	Trp	Leu	Ser	Leu	Gly	Gly
		115					120					125			
Phe	His	Glu	Arg	Gly	Gln	Asp	Trp	Glu	Gln	Thr	Gln	Lys	Ile	Tyr	Asn
	130					135					140				
Cys	His	Val	Leu	Leu	Asn	Ser	Lys	Gly	Ala	Val	Val	Ala	Thr	Tyr	Arg
145					150					155					160
Lys	Thr	His	Leu	Cys	Asp	Val	Glu	Ile	Pro	Gly	Gln	Gly	Pro	Met	Cys
				165					170					175	
Glu	Ser	Asn	Ser	Thr	Met	Pro	Gly	Pro	Ser	Leu	Glu	Ser	Pro	Val	Ser
			180				185						190		
Thr	Pro	Ala	Gly	Lys	Ile	Gly	Leu	Ala	Val	Cys	Tyr	Asp	Met	Arg	Phe
		195					200					205			
Pro	Glu	Leu	Ser	Leu	Ala	Leu	Ala	Gln	Ala	Gly	Ala	Glu	Ile	Leu	Thr
	210					215					220				
Tyr	Pro	Ser	Ala	Phe	Gly	Ser	Ile	Thr	Gly	Pro	Ala	His	Trp	Glu	Val
225					230					235					240
Leu	Leu	Arg	Ala	Arg	Ala	Ile	Glu	Thr	Gln	Cys	Tyr	Val	Val	Ala	Ala
				245					250					255	
Ala	Gln	Cys	Gly	Arg	His	His	Glu	Lys	Arg	Ala	Ser	Tyr	Gly	His	Ser
			260					265					270		
Met	Val	Val	Asp	Pro	Trp	Gly	Thr	Val	Val	Ala	Arg	Cys	Ser	Glu	Gly
		275					280					285			
Pro	Gly	Leu	Cys	Leu	Ala	Arg	Ile	Asp	Leu	Asn	Tyr	Leu	Arg	Gln	Leu
	290					295					300				
Arg	Arg	His	Leu	Pro	Val	Phe	Gln	His	Arg	Arg	Pro	Asp	Leu	Tyr	Gly
305					310					315					320
Asn	Leu	Gly	His	Pro	Leu	Ser									
				325											

<210> 22
 <211> 323
 <212> PRT
 <213> murine

<400> 22
 Met Leu Gly Phe Ile Thr Arg Pro Pro His Gln Leu Leu Cys Thr Gly
 1 5 10 15
 Tyr Arg Leu Leu Arg Ile Pro Val Leu Cys Thr Gln Pro Arg Pro Arg
 20 25 30
 Thr Met Ser Ser Ser Thr Ser Trp Glu Leu Pro Leu Val Ala Val Cys
 35 40 45
 Gln Val Thr Ser Thr Pro Asn Lys Gln Glu Asn Phe Lys Thr Cys Ala
 50 55 60
 Glu Leu Val Gln Glu Ala Ala Arg Leu Gly Ala Cys Leu Ala Phe Leu
 65 70 75 80
 Pro Glu Ala Phe Asp Phe Ile Ala Arg Asn Pro Ala Glu Thr Leu Leu
 85 90 95
 Leu Ser Glu Pro Leu Asn Gly Asp Leu Leu Gly Gln Tyr Ser Gln Leu

Ala	Arg	Glu	100	Cys	Gly	Ile	Trp	Leu	105	Ser	Leu	Gly	Gly	Phe	110	His	Glu	Arg
			115						120						125			
Gly	Gln	Asp	Trp	Glu	Gln	Asn	Gln	Lys	Ile	Tyr	Asn	Cys	His	Val	Leu			
			130						135						140			
Leu	Asn	Ser	Lys	Gly	Ser	Val	Val	Ala	Ser	Tyr	Arg	Lys	Thr	His	Leu			
			145												160			
Cys	Asp	Val	Glu	Ile	Pro	Gly	Gln	Gly	Pro	Met	Arg	Glu	Ser	Asn	Tyr			
				165						170					175			
Thr	Lys	Pro	Gly	Gly	Thr	Leu	Glu	Pro	Pro	Val	Lys	Thr	Pro	Ala	Gly			
			180							185					190			
Lys	Val	Gly	Leu	Ala	Ile	Cys	Tyr	Asp	Met	Arg	Phe	Pro	Glu	Leu	Ser			
			195							200					205			
Leu	Lys	Leu	Ala	Gln	Ala	Gly	Ala	Glu	Ile	Leu	Thr	Tyr	Pro	Ser	Ala			
			210							215					220			
Phe	Gly	Ser	Val	Thr	Gly	Pro	Ala	His	Trp	Glu	Val	Leu	Leu	Arg	Ala			
					230					235					240			
Arg	Ala	Ile	Glu	Ser	Gln	Cys	Tyr	Val	Ile	Ala	Ala	Ala	Gln	Cys	Gly			
				245						250					255			
Arg	His	His	Glu	Thr	Arg	Ala	Ser	Tyr	Gly	His	Ser	Met	Val	Val	Asp			
			260							265					270			
Pro	Trp	Gly	Thr	Val	Val	Ala	Arg	Cys	Ser	Glu	Gly	Pro	Gly	Leu	Cys			
			275							280					285			
Leu	Ala	Arg	Ile	Asp	Leu	His	Phe	Leu	Gln	Gln	Met	Arg	Gln	His	Leu			
			290							295					300			
Pro	Val	Phe	Gln	His	Arg	Arg	Pro	Asp	Leu	Tyr	Gly	Ser	Leu	Gly	His			
				310						315					320			
Pro	Leu	Ser																

<210> 23
 <211> 460
 <212> PRT
 <213> Drosophila melanogaster

<400> 23
 Met Ser Thr Leu Val Asn Thr Thr Arg Arg Ser Ile Val Ile Ala Ile
 1 5 10 15
 His Gln Gln Leu Arg Arg Met Ser Val Gln Lys Arg Lys Asp Gln Ser
 20 25 30
 Ala Thr Ile Ala Val Gly Gln Met Arg Ser Thr Ser Asp Lys Ala Ala
 35 40 45
 Asn Leu Ser Gln Val Ile Glu Leu Val Asp Arg Ala Lys Ser Gln Asn
 50 55 60
 Ala Cys Met Leu Phe Leu Pro Glu Cys Cys Asp Phe Val Gly Glu Ser
 65 70 75 80
 Arg Thr Gln Thr Ile Glu Leu Ser Glu Gly Leu Asp Gly Glu Leu Met
 85 90 95
 Ala Gln Tyr Arg Glu Leu Ala Lys Cys Asn Lys Ile Trp Ile Ser Leu
 100 105 110
 Gly Gly Val His Glu Arg Asn Asp Gln Lys Ile Phe Asn Ala His Val
 115 120 125
 Leu Leu Asn Glu Lys Gly Glu Leu Ala Ala Val Tyr Arg Lys Leu His
 130 135 140

Met	Phe	Asp	Val	Thr	Thr	Lys	Glu	Val	Arg	Leu	Arg	Glu	Ser	Asp	Thr
145					150					155					160
Val	Thr	Pro	Gly	Tyr	Cys	Leu	Glu	Arg	Pro	Val	Ser	Thr	Pro	Val	Gly
				165					170						175
Gln	Ile	Gly	Leu	Gln	Ile	Cys	Tyr	Asp	Leu	Arg	Phe	Ala	Glu	Pro	Ala
			180					185					190		
Val	Leu	Leu	Arg	Lys	Leu	Gly	Ala	Asn	Leu	Leu	Thr	Tyr	Pro	Ser	Ala
		195					200					205			
Phe	Thr	Tyr	Ala	Thr	Gly	Lys	Ala	His	Trp	Glu	Ile	Leu	Leu	Arg	Ala
	210					215					220				
Arg	Ala	Ile	Glu	Thr	Gln	Cys	Phe	Val	Val	Ala	Ala	Ala	Gln	Ile	Gly
225					230					235					240
Trp	His	Asn	Gln	Lys	Arg	Gln	Ser	Trp	Gly	His	Ser	Met	Ile	Val	Ser
			245						250					255	
Pro	Trp	Gly	Asn	Val	Leu	Ala	Asp	Cys	Ser	Glu	Gln	Glu	Leu	Asp	Ile
			260					265					270		
Gly	Thr	Ala	Glu	Val	Asp	Leu	Ser	Val	Leu	Gln	Ser	Leu	Tyr	Gln	Thr
		275					280					285			
Met	Pro	Cys	Phe	Glu	His	Arg	Arg	Asn	Asp	Ile	Tyr	Ala	Leu	Thr	Ala
	290					295					300				
Tyr	Asn	Leu	Arg	Ser	Lys	Glu	Pro	Thr	Gln	Asp	Arg	Pro	Phe	Ala	Thr
305					310					315					320
Asn	Ile	Val	Asp	Lys	Arg	Thr	Ile	Phe	Tyr	Glu	Ser	Glu	His	Cys	Phe
			325						330					335	
Ala	Phe	Thr	Asn	Leu	Arg	Cys	Val	Val	Lys	Gly	His	Val	Leu	Val	Ser
			340					345					350		
Thr	Lys	Arg	Val	Thr	Pro	Arg	Leu	Cys	Gly	Leu	Asp	Cys	Ala	Glu	Met
		355					360					365			
Ala	Asp	Met	Phe	Thr	Thr	Val	Cys	Leu	Val	Gln	Arg	Leu	Leu	Glu	Lys
	370					375					380				
Ile	Tyr	Gln	Thr	Thr	Ser	Ala	Thr	Val	Thr	Val	Gln	Asp	Gly	Ala	Gln
385					390					395					400
Ala	Gly	Gln	Thr	Val	Pro	His	Val	His	Phe	His	Ile	Met	Pro	Arg	Arg
			405						410					415	
Leu	Gly	Asp	Phe	Gly	His	Asn	Asp	Gln	Ile	Tyr	Val	Lys	Leu	Asp	Glu
			420					425					430		
Arg	Ala	Glu	Glu	Lys	Pro	Pro	Arg	Thr	Ile	Glu	Glu	Arg	Ile	Glu	Glu
		435					440					445			
Ala	Gln	Ile	Tyr	Arg	Lys	Phe	Leu	Thr	Asp	Ile	Ser				
450						455					460				

<210> 24
 <211> 440
 <212> PRT
 <213> C. elegans

<400> 24
 Met Leu Ser Thr Val Phe Arg Arg Thr Met Ala Thr Gly Arg His Phe
 1 5 10 15
 Ile Ala Val Cys Gln Met Thr Ser Asp Asn Asp Leu Glu Lys Asn Phe
 20 25 30
 Gln Ala Ala Lys Asn Met Ile Glu Arg Ala Gly Glu Lys Lys Cys Glu
 35 40 45
 Met Val Phe Leu Pro Glu Cys Phe Asp Phe Ile Gly Leu Asn Lys Asn

50	55	60
Glu Gln Ile Asp Leu Ala Met Ala Thr Asp Cys Glu Tyr Met Glu Lys		
65	70	75
Tyr Arg Glu Leu Ala Arg Lys His Asn Ile Trp Leu Ser Leu Gly Gly		80
	85	90
Leu His His Lys Asp Pro Ser Asp Ala Ala His Pro Trp Asn Thr His		95
	100	105
Leu Ile Ile Asp Ser Asp Gly Val Thr Arg Ala Glu Tyr Asn Lys Leu		110
	115	120
His Leu Phe Asp Leu Glu Ile Pro Gly Lys Val Arg Leu Met Glu Ser		125
	130	135
Glu Phe Ser Lys Ala Gly Thr Glu Met Ile Pro Pro Val Asp Thr Pro		140
145	150	155
Ile Gly Arg Leu Gly Leu Ser Ile Cys Tyr Asp Val Arg Phe Pro Glu		160
	165	170
Leu Ser Leu Trp Asn Arg Lys Arg Gly Ala Gln Leu Leu Ser Phe Pro		175
	180	185
Ser Ala Phe Thr Leu Asn Thr Gly Leu Ala His Trp Glu Thr Leu Leu		190
	195	200
Arg Ala Arg Ala Ile Glu Asn Gln Cys Tyr Val Val Ala Ala Ala Gln		205
	210	215
Thr Gly Ala His Asn Pro Lys Arg Gln Ser Tyr Gly His Ser Met Val		220
225	230	235
Val Asp Pro Trp Gly Ala Val Val Ala Gln Cys Ser Glu Arg Val Asp		240
	245	250
Met Cys Phe Ala Glu Ile Asp Leu Ser Tyr Val Asp Thr Leu Arg Glu		255
	260	265
Met Gln Pro Val Phe Ser His Arg Arg Ser Asp Leu Tyr Thr Leu His		270
	275	280
Ile Asn Glu Lys Ser Ser Glu Thr Gly Gly Leu Lys Phe Ala Arg Phe		285
	290	295
Asn Ile Pro Ala Asp His Ile Phe Tyr Ser Thr Pro His Ser Phe Val		300
305	310	315
Phe Val Asn Leu Lys Pro Val Thr Asp Gly His Val Leu Val Ser Pro		320
	325	330
Lys Arg Val Val Pro Arg Leu Thr Asp Leu Thr Asp Ala Glu Thr Ala		335
	340	345
Asp Leu Phe Ile Val Ala Lys Lys Val Gln Ala Met Leu Glu Lys His		350
	355	360
His Asn Val Thr Ser Thr Thr Ile Cys Val Gln Asp Gly Lys Asp Ala		365
	370	375
Gly Gln Thr Val Pro His Val His Ile His Ile Leu Pro Arg Arg Ala		380
385	390	395
Gly Asp Phe Gly Asp Asn Glu Ile Tyr Gln Lys Leu Ala Ser His Asp		400
	405	410
Lys Glu Pro Glu Arg Lys Pro Arg Ser Asn Glu Gln Met Ala Glu Glu		415
	420	425
Ala Val Val Tyr Arg Asn Leu Met		430
	435	440

<210> 25
 <211> 471
 <212> PRT
 <213> unknown

<220>
 <223> conserved sequence of human, murine, D.
 melanogaster and C. elegans Nit1

 <221> UNSURE
 <222> (6)...(6)
 <223> Xaa = unknown amino acid

 <221> SIGNAL
 <222> (363)...(363)
 <223> Xaa = stop signal

 <221> SIGNAL
 <222> (387)...(387)
 <223> Xaa = stop signal

 <221> SIGNAL
 <222> (403)...(403)
 <223> Xaa = stop signal

 <221> SIGNAL
 <222> (406)...(406)
 <223> Xaa = stop signal

 <221> SIGNAL
 <222> (420)...(420)
 <223> Xaa = stop signal

 <221> SIGNAL
 <222> (445)...(445)
 <223> Xaa = stop signal

 <221> SIGNAL
 <222> (451)...(451)
 <223> Xaa = stop signal

 <400> 25
 Pro Leu Ala Ala Ala Xaa Leu Ala Pro Asp Arg Pro Pro Asp Arg Thr
 1 5 10 15
 Leu Arg Met Val Leu Ala Ile Ser Ser Cys Arg Thr Tyr Ser Leu Ser
 20 25 30
 Arg Arg Pro Arg Leu Gly Phe Ile Thr Arg Pro Pro His Arg Phe Leu
 35 40 45
 Ser Leu Leu Cys Pro Gly Leu Arg Ile Pro Gln Leu Ser Val Leu Cys
 50 55 60
 Ala Gln Pro Arg Pro Arg Ala Met Ala Ile Ser Ser Ser Ser Cys Glu
 65 70 75 80
 Leu Pro Leu Val Ala Val Cys Gln Val Thr Ser Thr Pro Asp Lys Gln
 85 90 95
 Gln Asn Phe Lys Thr Cys Ala Glu Leu Val Arg Glu Ala Ala Arg Leu
 100 105 110
 Gly Ala Cys Leu Ala Phe Leu Pro Glu Ala Phe Asp Phe Ile Ala Arg
 115 120 125
 Asp Pro Ala Glu Thr Leu His Leu Ser Glu Pro Leu Gly Gly Lys Leu

130	135	140
Leu Glu Glu Tyr Thr Gln	Leu Ala Arg Glu Cys Gly	Leu Trp Leu Ser
145	150	155
Leu Gly Gly Phe His Glu	Arg Gly Gln Asp Trp Glu	Gln Thr Gln Lys
165	170	175
Ile Tyr Asn Cys His Val	Leu Leu Asn Ser Lys Gly	Ala Val Val Ala
180	185	190
Thr Tyr Arg Lys Thr His	Leu Cys Asp Val Glu Ile	Pro Gly Gln Gly
195	200	205
Pro Met Cys Glu Ser Asn	Ser Thr Met Pro Gly Pro	Ser Leu Glu Ser
210	215	220
Pro Val Ser Thr Pro Ala	Gly Lys Ile Gly Leu Ala	Val Cys Tyr Asp
225	230	235
Met Arg Phe Pro Glu	Leu Ser Leu Ala Leu	Ala Gln Ala Gly
245	250	255
Ile Leu Thr Tyr Pro	Ser Ala Phe Gly Ser	Ile Thr Gly Pro
260	265	270
Trp Glu Val Leu Leu	Arg Ala Arg Ala Ile	Glu Thr Gln Cys
275	280	285
Val Ala Ala Ala Gln	Cys Gly Arg His His	Glu Lys Arg Ala
290	295	300
Gly His Ser Met Val	Val Asp Pro Trp Gly Thr	Val Val Ala Arg
305	310	315
Ser Glu Gly Pro Gly	Leu Cys Leu Ala Arg	Ile Asp Leu Asn
325	330	335
Arg Gln Leu Arg Arg	His Leu Pro Val Phe	Gln His Arg Arg
340	345	350
Leu Tyr Gly Asn Leu	Gly His Pro Leu Ser	Xaa Asp Leu Thr
355	360	365
Ser Leu Asp Leu Pro	Leu Pro Pro Pro Cys	His Tyr Glu Leu
370	375	380
Leu Met Xaa Leu Gly	Gly Arg Ile Gln Ala	Gln Leu Pro Ser
385	390	395
Glu Pro Xaa Leu Ser	Xaa Trp Asn Thr Asp	Gly Leu Leu Gly
405	410	415
Thr Phe Thr Xaa Ala	Ser Pro Glu Val Arg	Leu Gln Phe Gln
420	425	430
Gly Ile Leu Tyr Ser	His Cys Leu Phe His	Gly Asn Xaa Ser
435	440	445
Glu Gly Xaa Ala Ala	Leu Ala Leu Lys	Asn Ile Ile Ile
450	455	460
Lys Lys Lys Lys Lys	Lys Lys	
465	470	